

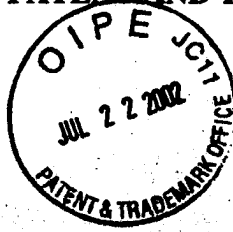
**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

**APPLICANT:** M. Jakobsen et al.

**SERIAL NO.:** 10/032,301

**FILED:** October 25, 2001

**FOR:** OPEN SUBSTRATE PLATFORM SUITABLE FOR ANALYSIS OF  
BIOMOLECULES



**THE HONORABLE COMMISSIONER OF PATENTS AND TRADEMARKS  
WASHINGTON, DC 20231**

**SIR:**

**PRELIMINARY AMENDMENT**

Please amend the above-identified application as follows.

**IN THE CLAIMS**

Please cancel without prejudice claims 5-17, 19-52 and 61-71.

18. (amended) The substrate of claim 1, which comprises immobilized nucleic acid sequences.

53. (amended) A method for identifying a nucleic acid sequence capable of binding to a biomolecule comprising:

immobilizing each unique nucleic acid sequence from a library of nucleic acid sequences onto the substrate platform of claim 1,

optionally washing the substrate platform to remove contaminants,

incubating the immobilized nucleic acid sequences with a biomolecule under conditions which are conducive to specific interaction between the biomolecule and the nucleic acid sequences,

optionally washing the substrate platform to remove any non-specifically bound biomolecules,

detecting the location of the nucleic acid sequences which bound to the biomolecule.

58. (amended) A method for identifying a polypeptide capable of binding to a biomolecule comprising:

immobilizing each unique polypeptide from a library of polypeptides onto the substrate platform of claim 1,

optionally washing the substrate platform to remove contaminants,

incubating the immobilized polypeptides with a biomolecule under conditions which are conducive to specific interaction between the biomolecule and the polypeptides,

optionally washing the substrate platform to remove any non-specifically bound biomolecules,

detecting the location of the polypeptides which bound to the biomolecule.

68. A method for sample analysis comprising:

applying a sample to the substrate platform of claim 1; and

evaluating the sample.

Please add the following new claims.

72. An open substrate platform comprising:

a slide element having opposing top and bottom surfaces,

wherein the top surface of the slide contains one or more depressions with a defined area for sample analysis,

wherein the bottom surface of the slide contains one or more depression opposing the depressions on the top surface.

73. An open substrate platform comprising:  
a slide element having opposing top and bottom surfaces, the slide element being substantially rectangular and formed from a plastic material, and  
wherein the top surface of the slide is comprised of a defined area for sample analysis;  
and  
wherein the bottom surface of the slide contains one or more depressions.

#### REMARKS

Applicants enclose herewith replacement pages 41-49 of the application. These replacement sheets correct inadvertent misnumbering of the claims as filed (claims numbered 18 and 23 was inadvertently omitted, i.e. the claims as filed progressed from claim 17 directly to claim 19 and from claim 22 directly to claim 24). The claim amendments made herein are based on the claim numbering as set forth on the enclosed replacement pages 41-49.

For the sole purpose of reducing initial claims fees, claims 5-17, 19-52 and 61-71 have been canceled without prejudice, and claims 18, 53, 58 and 68 have been amended. Applicants expressly reserve all rights to prosecute the subject matter of those cancelled and amended claims, either in the present application or suitable continuing application.

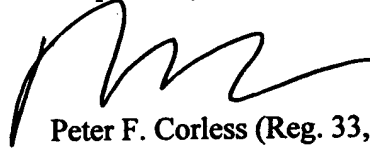
Claims 72 and 73 also have been added. No new matter has been added by virtue of those new claims. For instance, support for the new claims appears e.g. at page 10, lines 10-11 and original claims 1 and 4 of the application.

Applicants also submit herewith formal drawings for the application.

Early consideration and allowance of the application are earnestly solicited.

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Respectfully submitted,

A handwritten signature in black ink, appearing to be 'Peter F. Corless', written in a cursive style.

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**MARKED VERSION TO SHOW CHANGES**

18. (amended) The substrate of claim 1 [claims 1 or 4], which comprises immobilized nucleic acid sequences.

53. (amended) A method for identifying a nucleic acid sequence capable of binding to a biomolecule comprising:

immobilizing each unique nucleic acid sequence from a library of nucleic acid sequences onto the substrate platform of claim 1 [claims 1 or 4],

optionally washing the substrate platform to remove contaminants,

incubating the immobilized nucleic acid sequences with a biomolecule under conditions which are conducive to specific interaction between the biomolecule and the nucleic acid sequences,

optionally washing the substrate platform to remove any non-specifically bound biomolecules,

detecting the location of the nucleic acid sequences which bound to the biomolecule.

58. (amended) A method for identifying a polypeptide capable of binding to a biomolecule comprising:

immobilizing each unique polypeptide from a library of polypeptides onto the substrate platform of claim 1 [claims 1 or 4],

optionally washing the substrate platform to remove contaminants,

incubating the immobilized polypeptides with a biomolecule under conditions which are conducive to specific interaction between the biomolecule and the polypeptides,

optionally washing the substrate platform to remove any non-specifically bound biomolecules,

detecting the location of the polypeptides which bound to the biomolecule.

68. A method for sample analysis comprising:  
applying a sample to the substrate platform of claim 1 [claims 1 or 4]; and  
evaluating the sample.